

A METHOD FOR DETERMINING GENETIC AFFILIATION, SUBSTRUCTURE AND GENE FLOW WITHIN HUMAN POPULATIONS

ABSTRACT OF THE DISCLOSURE

The present invention provides novel polymorphisms on the Y chromosome and methods of using these polymorphisms as well as known polymorphisms on the Y chromosome as indicators of evolutionary heritage. The polymorphisms of the present invention are clustered to specific regions of the Y chromosome, and polymorphisms of particular use to the present methods are found in the non-recombining region of the human Y chromosome (NRY). These polymorphisms, including SNPs, insertions, and deletions, may be useful for numerous applications, including forensics, paternity testing, diagnosis and the like.

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